

SEQUENCE LISTING

<110> Schimmel, Paul
Wakasugi, Keisuke
Friedlander, Martin

<120> Tryptophanyl-tRNA Synthetase Derived
Polypeptides Useful For The Regulation of Angiogenesis

<130> TSRI-813.1

<150> 60/270,951

<151> 2001-02-23

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant human trpRS

<400> 1

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Glu	Glu	Asp	Phe	Val	Asp	Pro	Trp	Thr	Val	Gln	Thr	Ser	Ser	Ala	Lys
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Asp	Cys	Ile	Gly	Lys	Ile	Ser	Phe	Pro	Ala	Ile	Gln	Ala	Ala	Pro	Ser	
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Ser	Thr	Phe	Phe	Pro	Ala	Leu	Gln	Gly	Ala	Gln	Thr	Lys	Met	Ser	Ala	
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Glu	Glu	His	Arg	Gln	Phe	Gly	Gly	Asn	Cys	Asp	Val	Asp	Val	Ser	Phe	
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Arg	Lys	Asp	Tyr	Thr	Ser	Gly	Ala	Met	Leu	Thr	Gly	Glu	Leu	Lys	Lys	
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Arg	Lys	Glu	Val	Thr	Asp	Glu	Ile	Val	Lys	Glu	Phe	Met	Thr	Pro	Arg	
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Lys	Leu	Ser	Phe	Asp	Phe	Gln	Lys	Leu	Ala	Ala	Leu	Glu	His	His		
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant human mini-TrpRS in pET20B

<221> CDS
 <222> (3428)...(4738)

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 gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatgggtc 240
 acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

tgt cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc	3517
Cys Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala	
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aca gaa gct gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc	3565
Thr Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser	
35 40 45	
agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt	3613
Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser	
50 55 60	
agt aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc	3661
Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly	
65 70 75	
caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga	3709
Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg	
80 85 90	
gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat	3757
Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr	
95 100 105 110	
ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac	3805
Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His	
115 120 125	
ctc att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg	3853
Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val	
130 135 140	
ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac	3901
Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp	
145 150 155	
ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac	3949
Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp	
160 165 170	
atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac	3997
Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp	
175 180 185 190	
ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag	4045
Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys	
195 200 205	
att caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc	4093
Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe	
210 215 220	
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Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala	

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240	245	250	
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Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe			
255	260	265	270
aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc			4285
Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala			
275	280	285	
ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa			4333
Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys			
290	295	300	
atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc			4381
Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala			
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Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg			
320	325	330	
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Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp			
335	340	345	350
gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc			4525
Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu			
355	360	365	
gag cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag			4573
Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu			
370	375	380	
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Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His			
385	390	395	
cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg			4669
Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met			
400	405	410	
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Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu			
415	420	425	430
gag cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaag			4768
Glu His His His His His His			
435			
gaagctgagt tggctgctgc caccgctgag caataactag cataaccct tggggcctct			4828

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4877

<210> 3

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> human mini TrpRS in pET20B

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Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
35 40 45
Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
50 55 60
Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65 70 75 80
Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met
85 90 95
Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr
100 105 110
Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile
115 120 125
Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu
130 135 140
Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr
145 150 155 160
Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile
165 170 175
Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp
180 185 190
Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln
195 200 205
Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp
210 215 220
Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro
225 230 235 240
Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile
245 250 255
Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met
260 265 270
Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu
275 280 285
His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser
290 295 300
Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln
305 310 315 320
Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr
325 330 335
Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser
340 345 350

Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln
 355 360 365
 Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys
 370 375 380
 Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala
 385 390 395 400
 Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro
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<210> 4

<211> 4811

<212> DNA

<213> Artificial Sequence

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<223> Cleavage Product T1 of recombinant human TrpRS

<221> CDS

<222> (3428)...(4672)

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Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp

1

5

10

ttt gtg gac cca tgg aca gta cag aca agc agt gca aaa ggc ata gac 3517
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp
15 20 25 30

tac gat aag ctc att gtt cgg ttt gga agt agt aaa att gac aaa gag 3565
Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu
35 40 45

cta ata aac cga ata gag aga gcc acc ggc caa aga cca cac cac ttc 3613
Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe
50 55 60

ctg cgc aga ggc atc ttc ttc tca cac aga gat atg aat cag gtt ctt 3661
Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu
65 70 75

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80 85 90

ccc tct tct gaa gca atg cat gta ggt cac ctc att cca ttt att ttc 3757
Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe
95 100 105 110

aca aag tgg ctc cag gat gta ttt aac gtg ccc ttg gtc atc cag atg 3805
Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met
115 120 125

acg gat gac gag aag tat ctg tgg aag gac ctg acc ctg gac cag gcc 3853
Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala
130 135 140

tat ggc gat gct gtt gag aat gcc aag gac atc atc gcc tgt ggc ttt 3901
Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe
145 150 155

gac atc aac aag act ttc ata ttc tct gac ctg gac tac atg ggg atg 3949
Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met
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agc tca ggt ttc tac aaa aat gtg gtg aag att caa aag cat gtt acc 3997
Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr
175 180 185 190

ttc aac caa gtg aaa ggc att ttc ggc ttc act gac agc gac tgc att 4045
Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile
195 200 205

ggg aag atc agt ttt cct gcc atc cag gct gct ccc tcc ttc agc aac 4093
Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn
210 215 220

tca ttc cca cag atc ttc cga gac agg acg gat atc cag tgc ctt atc 4141
Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile
225 230 235

cca tgt gcc att gac cag gat cct tac ttt aga atg aca agg gac gtc 4189
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
240 245 250

gcc ccc agg atc ggc tat cct aaa cca gcc ctg ttg cac tcc acc ttc 4237
Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe
255 260 265 270

ttc cca gcc ctg cag ggc gcc cag acc aaa atg agt gcc agc gac cca 4285
Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro
275 280 285

aac tcc tcc atc ttc ctc acc gac acg gcc aag cag atc aaa acc aag 4333
Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys
290 295 300

gtc aat aag cat gcg ttt tct gga ggg aga gac acc atc gag gag cac 4381
Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His
305 310 315

agg cag ttt ggg ggc aac tgt gat gtg gac gtg tct ttc atg tac ctg 4429
Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu

320

325

330

acc ttc ttc ctc gag gac gac gac aag ctc gag cag atc agg aag gat 4477
 Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp
 335 340 345 350

tac acc agc gga gcc atg ctc acc ggt gag ctc aag aag gca ctc ata 4525
 Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile
 355 360 365

gag gtt ctg cag ccc ttg atc gca gag cac cag gcc cgg cgc aag gag 4573
 Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu
 370 375 380

gtc acg gat gag ata gtg aaa gag ttc atg act ccc cgg aag ctg tcc 4621
 Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser
 385 390 395

ttc gac ttt cag aag ctt gcg gcc gca ctc gag cac cac cac cac cac 4669
 Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His
 400 405 410

cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt tggtctgctgc 4722
 His
 415

caccgctgag caataactag cataaccct tggggcctct aaacgggtct tgagggggtt 4782
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<210> 5

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage Product T1 of recombinant human TrpRS

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 Lys Leu Ile Val Arg Phe Gly Ser Lys Ile Asp Lys Glu Leu Ile
 35 40 45
 Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg
 50 55 60
 Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala
 65 70 75 80
 Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser
 85 90 95
 Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys
 100 105 110
 Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp
 115 120 125
 Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly

130	135	140	
Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile			
145	150	155	160
Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser			
	165	170	175
Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn			
	180	185	190
Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys			
	195	200	205
Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe			
	210	215	220
Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys			
	225	230	235
Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro			
	245	250	255
Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro			
	260	265	270
Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser			
	275	280	285
Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn			
	290	295	300
Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln			
	305	310	315
Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe			
	325	330	335
Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr			
	340	345	350
Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val			
	355	360	365
Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr			
	370	375	380
Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp			
	385	390	395
Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His			
	405	410	415

<210> 6

<211> 4742

<212> DNA

<213> Artificial Sequence

<220>

<223> Cleavage Product T2 of recombinant human TrpRS

<221> CDS

<222> (3428)...(4603)

<400> 6

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ctttctcgcc acgttcgccc gctttccccg tcaagctcta aatcgggggc tccctttagg 180
gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatgggtc 240
acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300
ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggctctattc 360

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Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe	
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tca cac aga gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag	3613
Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys	
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cca ttt tat ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat	3661
Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His	
65 70 75	
gta ggt cac ctc att cca ttt att ttc aca aag tgg ctc cag gat gta	3709
Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val	
80 85 90	
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Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu	
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Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn	
115 120 125	
gcc aag gac atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata	3853
Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile	
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ttc tct gac ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat	3901
Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn	
145 150 155	
gtg gtg aag att caa aag cat gtt acc ttc aac caa gtg aaa ggc att	3949
Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile	
160 165 170	
ttc ggc ttc act gac agc gac tgc att ggg aag atc agt ttt cct gcc	3997
Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala	
175 180 185 190	
atc cag gct gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga	4045
Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg	
195 200 205	
gac agg acg gat atc cag tgc ctt atc cca tgt gcc att gac cag gat	4093
Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp	
210 215 220	
cct tac ttt aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct	4141
Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro	
225 230 235	

aaa cca gcc ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc 4189
 Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala
 240 245 250

cag acc aaa atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc 4237
 Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr
 255 260 265 270

gac acg gcc aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct 4285
 Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser
 275 280 285

gga ggg aga gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt 4333
 Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys
 290 295 300

gat gtg gac gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac 4381
 Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp
 305 310 315

gac aag ctc gag cag atc agg aag gat tac acc agc gga gcc atg ctc 4429
 Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu
 320 325 330

acc ggt gag ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc 4477
 Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile
 335 340 345 350

gca gag cac cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa 4525
 Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys
 355 360 365

gag ttc atg act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg 4573
 Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala
 370 375 380

gcc gca ctc gag cac cac cac cac cac tgagatccgg ctgctaacaa 4623
 Ala Ala Leu Glu His His His His His His
 385 390

agcccgaag gaagctgagt tggctgctgc caccgctgag caataactag cataaccct 4683
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<210> 7

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage Product T2 of recombinant human TrpRS

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 35 40 45
 Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe
 50 55 60
 Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly
 65 70 75 80
 His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn
 85 90 95
 Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys
 100 105 110
 Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys
 115 120 125
 Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser
 130 135 140
 Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val
 145 150 155 160
 Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly
 165 170 175
 Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln
 180 185 190
 Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg
 195 200 205
 Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr
 210 215 220
 Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro
 225 230 235 240
 Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr
 245 250 255
 Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr
 260 265 270
 Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly
 275 280 285
 Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val
 290 295 300
 Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys
 305 310 315 320
 Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly
 325 330 335
 Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu
 340 345 350
 His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe
 355 360 365
 Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala
 370 375 380
 Leu Glu His His His His His His
 385 390

<210> 8

<211> 5

<212> PRT

<213> Homo sapiens

<400> 8
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<210> 9
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 <212> PRT
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<400> 9
 Ser Ala Lys Gly Ile
 1 5

<210> 10
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 His Val Gly His
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<210> 11
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<400> 11
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<210> 12
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<400> 12
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 35 40 45
 Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr
 50 55 60
 Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His
 65 70 75 80
 Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val
 85 90 95
 Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp
 100 105 110

Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp
 115 120 125
 Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp
 130 135 140
 Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys
 145 150 155 160
 Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe
 165 170 175
 Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala
 180 185 190
 Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr
 195 200 205
 Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
 210 215 220
 Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala
 225 230 235 240
 Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys
 245 250 255
 Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala
 260 265 270
 Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg
 275 280 285
 Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp
 290 295 300
 Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu
 305 310 315 320
 Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu
 325 330 335
 Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His
 340 345 350
 Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met
 355 360 365
 Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln
 370 375

<210> 13
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 13
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 Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn
 35 40 45
 Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg
 50 55 60
 Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr
 65 70 75 80
 Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser
 85 90 95
 Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp

